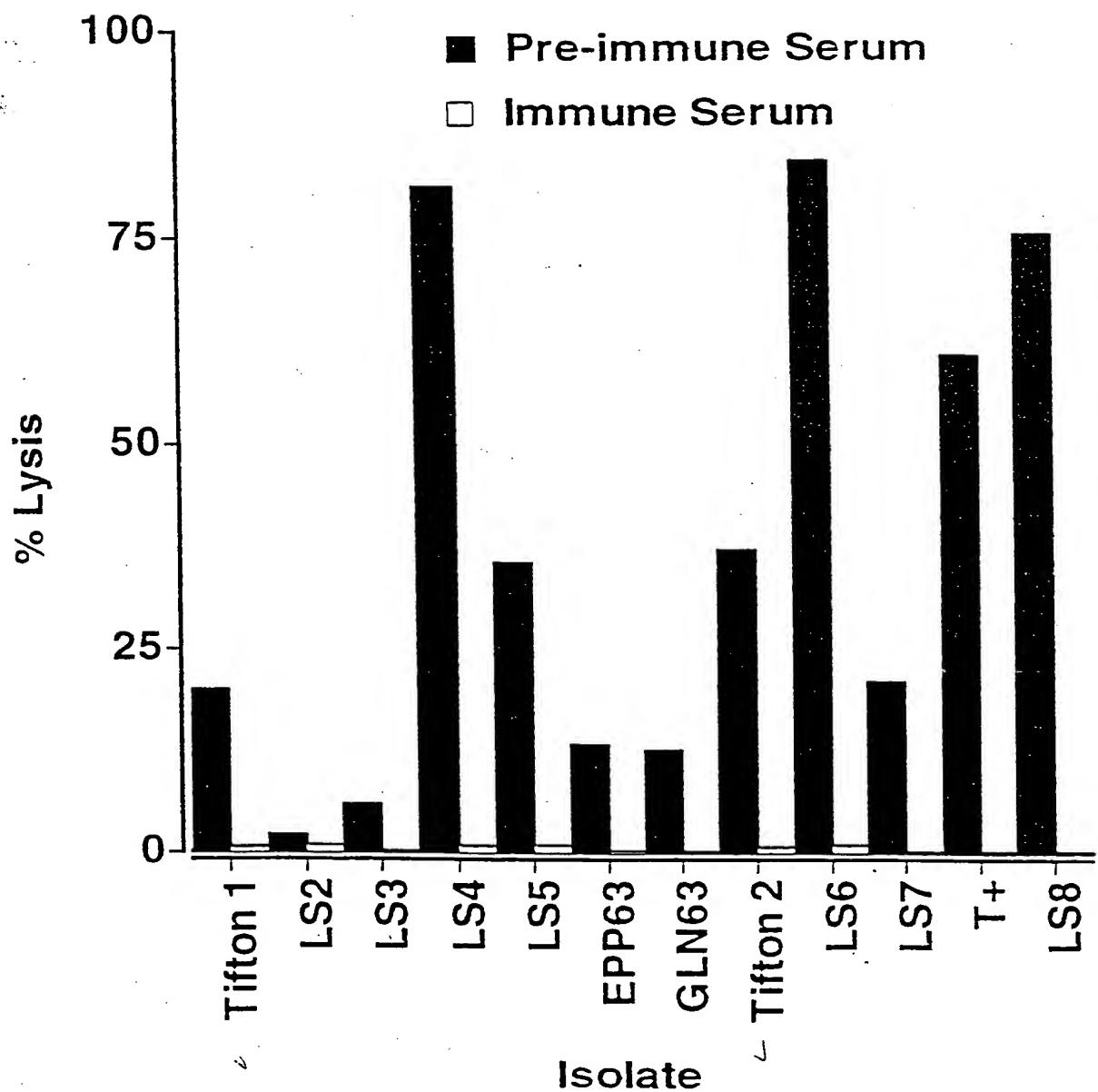


#5

FIG. 1



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FIG. 2

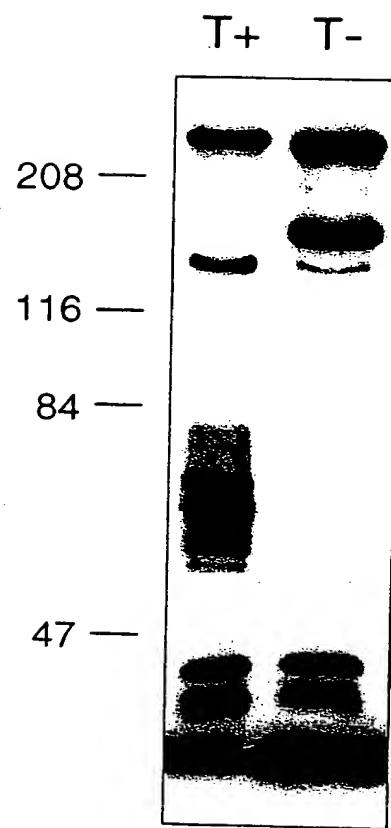


FIG 3-1

Appendix A update-July 1999

Bases 1-1200

Amino acids 1-400

1 ATGTCCAATATAAATGTAATTAAATCTAATATTCAAGCAGGCTTGAATTCAACAAAGTCT	60
1 M S N I N V I K S N I Q A G L N S T K S	20
61 GGATTAAGGGAAATCTTACTTGGCTATTCCAAAGATTATGATCGCAAAAGGTGGACT	120
21 G L K N L Y L A I P K D Y D P Q K G G T	40
121 TTAAATGATTTATTAAAGCTGCTGATGAATTAGGTATTGCTCGTTAGCAGAAGAGCCT	180
41 L N D F I K A A D E L G I A R L A E E P	60
181 AATCACACTGAAACAGCAAAAAATCTGTTGACACAGTAAATCAGTTCTCTCTCACA	240
61 N H T E T A K K S V D T V N Q F L S L T	80
241 CAAACTGGTATTGCTATTCGCAACAAAATTAGAAAAGTCTTACAAAACATTCTACC	300
81 Q T G I A I S A T K L E K F L Q K H S T	100
301 AATAAGTTAGCAAAGGGTTAGACAGTGTAGAAAATATTGATCGTAAATTAGTAAAGCA	360
101 N K L A K G L D S V E N I D R K L G K A	120
361 AGTAATGTATTATCACATTAAGCTTTGGGCACTGCATTAGCGGGTATAGAACCTT	420
121 S N V L S T L S S F L G T A L A G I E L	140
421 GATTCTTAATCAAAAAGGTGATGCTGCACCTGATGCTTGGCTAAAGCTAGTAGTATTGAC	480
141 D S L I K K G D A A P D A L A K A S I D	160
481 TTGATTAATGAGATAATTGGTAATCTATCTCAGAGTACTCAAACGATTGAAGCATTCT	540
161 L I N E I I G N L S Q S T Q T I E A F S	180
541 TCACAGTTAGCAAAGTTAGGTTCTACTATATCGCAGGCTAAAGGTTCTCTAAATAGGA	600
181 S Q L A K L G S T I S Q A K G F S N I G	200
601 AACAAAGTTGCAAAACTAAATTCTAAACAAATCTGGTTGGAAATAATTACTGGT	660
201 N K L Q N L N F S K T N L G L E I I T G	220
661 TTGCTATCAGGCATTCTGCAGGCTTGCTTAGCGGATAAAAATGCATCGACTGGCAAA	720
221 L L S G I S A G F A L A D K N A S T G K	240
721 AAAGTTGCTGCAGGTTTGATTAAGCAATCAAGTTATTGTAATGTAACAAAGCAATT	780
241 K V A A G F E L S N Q V I G N V T K A I	260
781 TCTTCATATGTTTAGCACAACGTGTTGCTGGTCTATCAACTACTGGTGTGCTGGCT	840
261 S S Y V L A Q R V A A G L S T T G A V A	280
841 GCTTTAATTACTTCATCGATTATGTTGGCAATTAGTCCTTGGCATTTATGAATGCAGCA	900
281 A L I T S S I M L A I S P L A F M N A A	300
901 GATAAATTCAATCATGCTAATGCTTGTAGTGGTAAACAAATTCCGAAAATTGGC	960
301 D K F N H A N A L D E F A K Q F R K F G	320
961 TATGATGGGATCATTATTGGCTGAATATCAGCGTGGTGGTACTATTGAAGCTTCA	1020
321 Y D G D H L L A E Y Q R G V G T I E A S	340
1021 TTAACTACAATTAGTACGGCATTAGGTGCAGTTCTGCTGGTGTGCTGCTGTA	1080
341 L T T I S T A L G A V S A G V S A A A V	360
1081 GGATCTGCTGTTGGTGCACCGATTGCACTATTAGTTGCAGGTGTTACAGGATTGATCTCT	1140
361 G S A V G A P I A L L V A G V T G L I S	380
1141 GGAATTAGAAGCGTCTAACACAGGCAATGTTGAAAGTGTGCTAACCGTTACAAGGT	1200
381 G I L E A S K Q A M F E S V A N R L Q G	400

FIG 3-2

Appendix A update-July 1999, continued

Bases 1201-2400
Amino acids 401-800

1201	AAAATTTAGAGTGGAAAAGCAAAATGGCGGTAGAACTATTTGATAAAGGCTATGAT	1260
401	K I L E W E K Q N G G Q N Y F D K G Y D	420
1261	TCTCGTTATGCTGCTTATTAGCTAATAACTAAAATTTGAGCTAAATAAGAG	1320
421	S R Y A A Y L A N N L K F L S E L N K E	440
1321	TTGGAAGCTGAACGTGTTATTGCAATCACCAACAAACGTTGGGATAATAATTGGTGAG	1380
441	L E A E R V I A I T Q Q R W D N N I G E	460
1381	TTAGCAGGTATTACCAAATTGGGTGAACGCATTAAGAGCGAAAAGCTTATGCAGATGCT	1440
461	L A G I T K L G E R I K S G K A Y A D A	480
1441	TTTGAAGATGGCAAGAAAGTTGAAGCTGGTCCAATATTACTTGGATGCTAAACTGGT	1500
481	F E D G K K V E A G S N I T L D A K T G	500
1501	ATCATAGACATTAGTAATTCAAATGGAAAAAACGCAAGCGTTGCATTCACCGCCT	1560
501	I I D I S N S N G K K T Q A L H F T S P	520
1561	TTGTTAACAGCAGGAACGTAAATCACGTGAACGTTAACTAATGGTAAATACTCTTATATT	1620
521	L L T A G T E S R E R L T N G K Y S Y I	540
1621	AATAAGTTAAATTGGACGTGAAAAACTGGCAAGTTACAGATGGAGAGGCTAGTTCT	1680
541	N K L K F G R V K N W Q V T D G E A S S	560
1681	AAATTAGATTCTCTAAAGTTATTCAACGTGAGCCGAGACAGAAGGCACAGACGAGATT	1740
561	K L D F S K V I Q R V A E T E G T D E I	580
1741	GGTCTAATAGTAAATGCAAAAGCTGGCAATGACGATATCTTGTGGTCAAGGTAAATG	1800
581	G L I V N A K A G N D D I F V G Q G K M	600
1801	AATATTGATGGTGGAGATGGACACGATCGTCTTCTATAGTAAAGACGGAGGATTGGT	1860
601	N I D G G D G H D R V F Y S K D G G F G	620
1861	AATATTACTGTAGATGGTACGAGTGCAACAGAACAGCAGGTTATACAGTTAATCGTAAG	1920
621	N I T V D G T S A T E A G S Y T V N R K	640
1921	GTTGCTCGAGGTGATATCTACCATGAAGTTGTGAAGCGTCAAGAAACCAAGGTGGTAAA	1980
641	V A R G D I Y H E V V K R Q E T K V G K	660
1981	CGTACTGAAACTATCCAGTATCGTATTGAATTAAGAAAAGTTGGTATGGTATCAG	2040
661	R T E T I Q Y R D Y E L R K V G Y G Y Q	680
2041	TCTACCGATAATTGAAATCAGTAGAGAAGTAATTGGTCTCAATTAAATGATGTATT	2100
681	S T D N L K S V E E V I G S Q F N D V F	700
2101	AAAGGTTCTAAATTCAACGACATATTCCATAGTGGTGAAGGTGATGATTACTCGATGGT	2160
701	K G S K F N D I F H S G E G D D L L D G	720
2161	GGTGTGGTGACGACCGCTTGTGGTAAAGGCAACGATCGACTTCTGGAGATGAA	2220
721	G A G D D R L F G G K G N D R L S G D E	740
2221	GGCGATGATTTACTCGATGGCGTTCTGGTATGATGTATTAAATGGTGGTCTGGTAAT	2280
741	G D D L L D G G S G D D V L N G G A G N	760
2281	GATGTCTATATCTTCGAAAGGTGATGGAATGATACTTGTACGATGGCACGGCAAT	2340
761	D V Y I F R K G D G N D T L Y D G T G N	780
2341	GATAAATTAGCATTTGCAAGATGCAAATATATCTGATATTATGATTGAACTGACCAAAGAG	2400
781	D K L A F A D A N I S D I M I E R T K E	800

FIG 3-3

Appendix A update-July 1999, continued

Bases 2401-2784

Amino acids 801-927

2401	GGTATTATAGTTAACGAAATGATCATTAGGTAGTATTAACATACCAAGATGGTACATA	2460
801	G I I V K R N D H S G S I N I P R W Y I	820
2461	ACATCAAATTACAAAATTATCAAAGTAATAAAACAGATCATAAAATTGAGCAACTAATT	2520
821	T S N L Q N Y Q S N K T D H K I E Q L I	840
2521	GGTAAAGATGGTAGTTATATCACTTCCGATCAAATTGATAAAATTGGCAAGATAAGAAA	2580
841	G K D G S Y I T S D Q I D K I L Q D K K	860
2581	GATGGTACAGTAATTACATCTAAGAATTGAAAAAGCTTGCTGATGAGATAAGAGCAA	2640
861	D G T V I T S Q E L K K L A D E N K S Q	880
2641	AAATTATCTGCTTCGGACATTGCAAGTAGCTTAAATAAGCTAGTTGGTCAATGGCACTA	2700
881	K L S A S D I A S S L N K L V G S M A L	900
2701	TTTGGTACAGCAAATAGTGTGAGTTCAACGCCCTACAGCCAATTACACAACCAACTCAA	2760
901	F G T A N S V S S N A L Q P I T Q P T Q	920
2761	GGAATTTGGCTCCAAGTGTAG	SEQ ID NO: 1
921	G I L A P S V *	SEQ ID NO: 2

F16.4

FIG.5

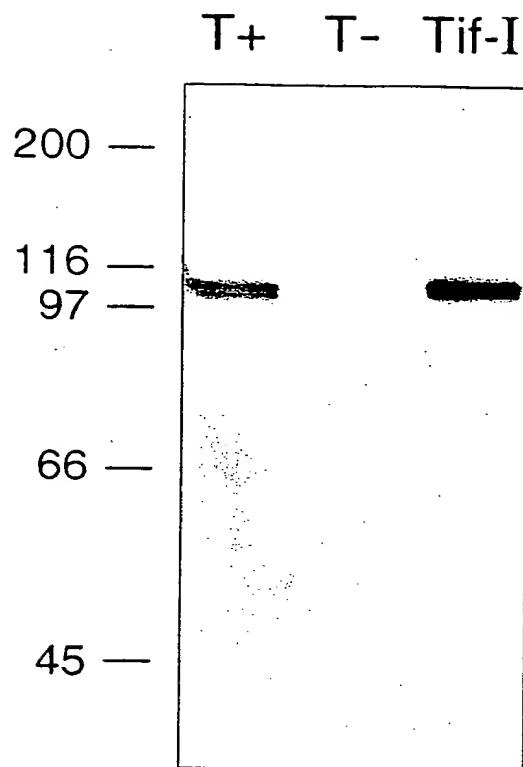
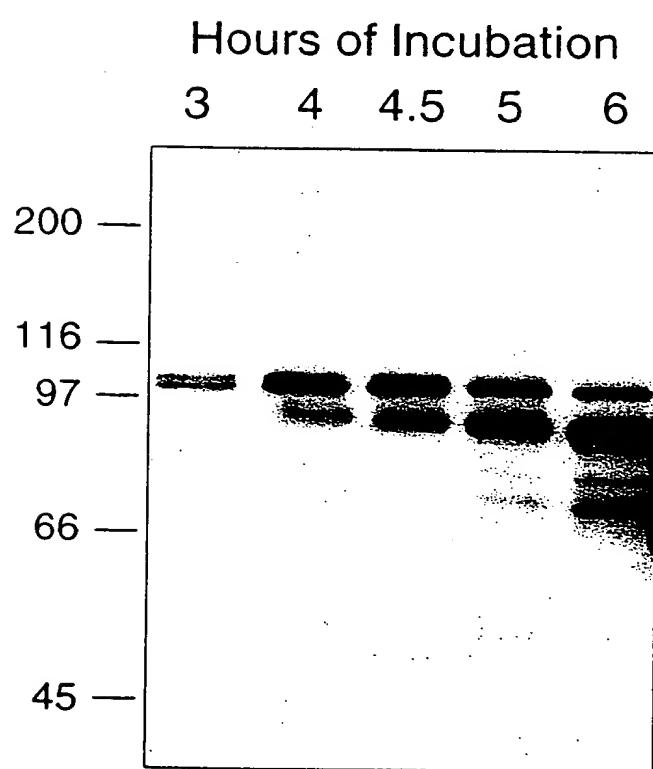
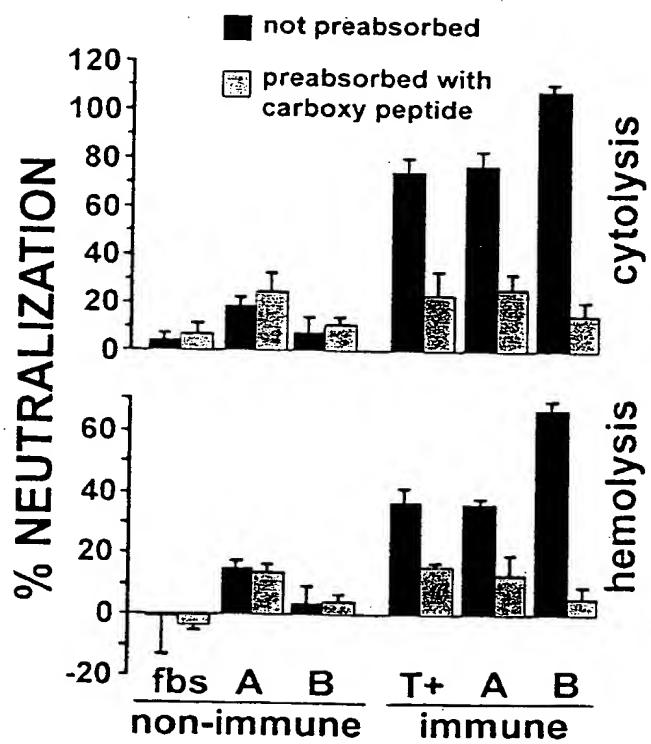


FIG.6



F16.7



UNASIS TRANSLATION EDITION LII-000 D year. unu			
1 ATGGGTGGTGAATCTCTTAATTAGACTTAATTTACAAACCTTAATAGTAATTTAGTT	60		8-1
1 M G G D T S L I R N L Q T L N S N L V			
61 ATGATAGATTATGCTCAACAACCTGCTCATCTGCTCTGGTTATCCTTGCAAATACTAT	120		
21 M I D Y A Q Q P A L S A L V I L A K Y Y	40		
121 GGTATTTCTGCAAGTCCAGCAGACATTATGCATCAGTTTCTGATAATACAAAAGGAGAC	180		
41 G I S A S P A D I M H Q F S D N T K G D	60		
181 CTGAATGAAATTGAATGGATGTTGGCAGCAAAGAAATTAGAATTAAGGTAAAGGATTATA	240		
61 L N E I E W M L A A K K L E L K V K I I	80		
241 AACAGCCTTAACTCGATTGTCAATGATAACACTTCCTGCTTGGTGTGGTGTGATAAT	300		
81 K Q P L T R L S M I T L P A L V W C D N	100		
301 AAGCCGATTAGATCAAAATTAAACTCTCATTTATACACTAACTAAAATTGATGGGTG	360		
101 K P D L D Q N L N S H F I L T K I D G V	120		
361 GGATCTGCTGAAAATATCTCATCTACGATTGATTGAGAATCGTCCCATAATATTAGAT	420		
121 G S A A K Y L I Y D L I E N R P I I L D	140		
421 GCAAGTGAGTTCTGAAAGATATTCTGTAAGTTAATGCTAGTAACCTCCGTGCGTCA	480		
141 A S E F S E R Y S G K L M L V T S R A S	160		
481 ATATTGGTTCATGGCTAAATTGATTACTTGGTTATTCTGCGGTAAATCAAATAT	540		
161 I L G S L A K F D F T W F I P A V I K Y	180		
541 CGTTATATTTTTGAAGTCATCGTTATTCACTGGTGTACAGATTGCTCTGATT	600		
181 R Y I F F E V I V I S V V L Q I F A L I	200		
601 ACGCCATTGTTTCAAGTTGTGATGGATAAGGTATTGGTGCATCGTGGTTTCTACT	660		
201 T P L F F Q V V M D K V L V H R G F S T	220		
661 CTGGATGTGGTAGCGATTGCCCTGGTAGTAAGTTATTGAAGTCATTAAAGTGGT	720		
221 L D V V A I A L L V V S L F E V I L S G	240		
721 CTACGCACTTATATTTGCTCATACAAACCTCTGAATTGATGTAGAGCTAGGAGCACGA	780		
241 L R T Y I F A H T T S R I D V E L G A R	260		
781 TTATTCGTCATCTATTAGCTACCGCTTGGTTAGAGTAGAAGAGTAGGGCGAT	840		
261 L F R H L L A L P L A Y F E S R R V G D	280		
841 ACAGTTGCACTACGTGAATTGGAACATATCCGCAATTCTTAACGGTCAAGCTCTC	900		
281 T V A R I R E L E H I R N F L T G Q A L	300		
901 ACTTCAGTTAGATTGGTGTCTTATATTCTGTTGTAATGTGGTATTACAGC	960		
301 T S V L D L V F S F I F L F V M W Y Y S	320		
961 CCTACTTAAACACTGGTAGTTGGCATCATTACCAATATGCGTTGGTCTGCTT	1020		
321 P T L T L V V L A S L P I Y A F W S A F	340		
1021 ATTAGCCAATTACGCACCGACTAAATGATCAATTGCACTCGCAATGCGAGATAATCAA	1080		
341 I S P I L R T R L N D Q F A R N A D N Q	360		
1081 TCTTTTTAGTGGAAAGTATTACTGGGGTTGGTAGGGTAAAGCAATGGCAGTTGAACCT	1140		
361 S F L V E S I T A V G T V K A M A V E P	380		
1141 CAAATGACCGTCGGGATAATCAATTAGCAGCTTATGTGGTTCTAGTTGGGTAA	1200		
381 Q M T R R W D N Q L A A Y V V S S F R V	400		
1201 GCTAAGTTGGCAATGGGGCAGCAAGGAGTACAACCTCATCAAAAGATGGTTATTGTG	1260		
401 A K L A M V G Q Q G V Q L I Q K M V I V	420		
1261 GCAACTCTATGGATTGGTCAAAATTGTAATTGAAGGCAAGCTATGGTAGGTCAATT	1320		
421 A T L W I G A K L V I E G K L S V G Q L	440		

DNA sequence		Start position	End position
1321	ATAGCATTTAATATGCTGGCAGGTAGGTGGCCGCTCTGTTATCGCCTGGCACAGCTA		1380
441	I A F N M L A G Q A A P V I R L A Q L		
1381	TGGCAAGATTTCAAGCAAGTAGGTATTCACTGGGAGATTGGGTGATATTTAAACT		1440
461	W Q D F Q Q V G I S V A R L G D I L N T		480
1441	CCAAC TGAGCATTCTACATCTCGCTTAACCTTACCTGATATTAAGGGTGATATTACATT		1500
481	P T E H S T S R L T L P D I K G D I T F		500
1501	GAAAATGTTGATTTTCGCTACAAAATAGATGGGCATTAAATATTACAGAATTAAATT		1560
501	E N V D F R Y K I D G H L I L Q N L N L		520
1561	CAGATTAACGCTGGAGAGATACTAGGTATCGTAGGACGCTCTGGTTCAAGTAAATCAACA		1620
521	Q I N A G E I L G I V G R S G S G K S T		540
1621	TTGACAAAATTAGTACAGCGTTATATGTACCAAGAAAATGGCGAATATTAGTTGATGGA		1680
541	L T K L V Q R L Y V P E N G R I L V D G		560
1681	AACGATTGCGATTAGCTGATCCCGCTGGCTGCGTCGCCAAGTGGGTGTTGTTGCAG		1740
561	N D L A L A D P A W L R R Q V G V V L Q		580
1741	GAAAATGTGTTACTCAATCGTAGTATTGAGATAATATTGCCCTAACGTACACGGGATG		1800
581	E N V L L N R S I R D N I A L T D T G M		600
1801	TCATTAGAGTTTATTATCCAGGCTGCCAAGATGCTGGGGCACATGACTTTATTATGGAA		1860
601	S L E F I I Q A A K M S G A H D F I M E		620
1861	TTGCCCTGAGGGTTATGATACGATTGTTGGAGAGCAAGGTGCAGGCTTGTCAAGGTGGACAA		1920
621	L P E G Y D T I V G E Q G A G L S G G Q		640
1921	CGCCAGCGTATCGTATTGCGCGTCTTAATTACCAATCCCGTATTTGATTTTGAT		1980
641	R Q R I A I A R A L I T N P R I L I F D		660
1981	GAAGCTACTAGTCGATTAGACTATGAGTCGGAAAGGGCTATTATGCAAAATATGCAGGCA		2040
661	E A T S A L D Y E S E R A I M Q N M Q A		680
2041	ATTTGCCAAGGTAGAACAGTGTGATTATTGCACATCGCTTATCTACCGTAAAAATGGCA		2100
681	I C Q G R T V L I I A H R L S T V K M A		700
2101	CATCGCATTATTGCAATGGACAAGGGAAAATTGTAGAGCAAGGCACACATCAAGAATTG		2160
701	H R I I A M D K G K I V E Q G T H Q E L		720
2161	TTGCAAAAGAAGATGGTTACTATCGTTATATGATTGAGAATGGATAAA		2215
721	L Q K E D G Y Y R Y L Y D L Q N G *		739

F16.8-2

F16.9

MbxB	-----MID	Y A Q Q P A L S A	L V I L A K Y Y C	I S A S P A I H	H Q P S D N T K G	D L N E I E W M L	A A K K L H E	55
LktB	M A N B O R N D	L G L V A	L T M L A Q Y H S	I S L E P E E I K	H K F D L D G R G	E L S L T A W L L	A A K S L A L	56
ApxIB	K D F Y R E . E D	Y G L Y A	L T I L A Q Y H S	I A V E P E E R	H K P D L G K G	E L D L T A W L L	A A K S L E E	55
HlyB	M D S C H K . E D	Y G L Y A	L E I L A Q Y H S	I S V E P E E I K	H I P D T D G T G	E L G L T S W L L	A A K S L B E	55
MbxB	R U X I I Q P T	T H E S M I T L P	A L V W C D N K P	D L D Q N L N S H	F I L T K I D G V	G S R A K Y L I Y	D L I T N R P	116
LktB	N A R H I K N E I	S B L H L N L P	A L V W Q Q D N	F I L T K I D . . .	T N H R Y I L T Y	N L E Q D A E	107
ApxIB	K A K Q V K K A X	D R L A P I A L P	A L V W R E D	F I L T K I D . . .	N E A K K Y I L I F	D L E T H N F	106
HlyB	K V K Q V K R K T I	D R E N P I S L P	A L V W R E D	F I L T R V S . . .	K E A N R Y I L F	D L E Q R N F	106
MbxB	I I L M A S E P S	E R Y S G K L H M L	V T S R A S I L G	S L A K P D F T W	F I P A V I K Y R	Y I F P E V V V V	S V V L Q L F	177
LktB	Q I L S T D E P E	A C Y V Q G Q L M L	V T S R A S I V V G	S L A K P D F T W	F I P A V I K Y R	Y I F P E T T L I V V	S I P L Q I F	168
ApxIB	R I L E Q A R P E	S L Y Q C K L L I L	V A S R A S I V G	S L A K P D F T W	F I P A V I K Y R	Y I F P E T T L I V V	S I P L Q I F	167
HlyB	R I L E Q S E P E	A L Y Q G H . I L	V A S R S B V A G	S L A K P D F T W	F I P A V I K Y R	Y I F P E T T L I V V	S V P L Q . P	167
MbxB	A L I T P L F F Q	V V M D K V L V B	R G F S T L D V	A . A L L V V S L	F E . I L S G L R	T Y I F A H T T S	R I D V E L G	238
LktB	A L I T P L F F Q	V V M D K V L V B	R G F S T L H N I	T V A L A I V . .	F R I V I L S G L R	T Y . P S R S T S	R I D V E L G	229
ApxIB	A L I T P L F F Q	V V M D K V L V B	R G F S T L H V I	T V A L A I V V L	F R I V I L A C L R	T Y I F A H S T S	R I D V E L G	228
HlyB	A L I T P L F F Q	V V M D K V L V B	R G F S T L N V I	T V A L S V V V V	F R I V I L S G L R	T Y I F A H S T S	R I D V E L G	228
MbxB	A R L P R H L L A	L P T A X P E S R	R V G D T V A R	R E L D H I R H F	L T G Q A L T S V	L D L V F S P I F	L F V M W X Y	299
LktB	A K L P R H L L S	L P I S Y P E N R	R V G D T V A R V	R E L D Q I R H F	L T G Q A L T S V	L D L L F S P I F	P A V M W X Y	290
ApxIB	A R L P R H L L A	L P I S Y P E N R	R V G D T V A R V	R E L D Q I R H F	L T G Q A L T S V	L D L L F S P I F	P A V M W X Y	289
HlyB	A K L P R H L L A	L P I S Y P E S R	R V G D T V A R V	R E L D Q I R H F	L T G Q A L T S V	L D L L F S P I F	P A V M W X Y	289
MbxB	S P A L T L V L	A S L P I K A F W	S A F I S P I L R	T R L N D O P A R	H A D N Q S P L V	E S T A T I G T	K A M A V E P	360
LktB	S P K L T L V I L	G S L P C Z I L W	S I F I S P I L R	T R L L D E K F A R	S A D H Q A P L V	R S V T A I N M I	K A M A V A P	351
ApxIB	S P K L T L V I L	G S L P F Y M G W	S I F I S P I L R	T R L L D E K F A R	G A D H Q S P L V	R S V T A I S T I	K A M A V T P	350
HlyB	S P K L T L V I L	F S L P C Y A W W	S I F I S P I L R	T R L L D D K F S R	N A D H Q S P L V	R S V T A I N T I	K A M A V S P	350
MbxB	Q M T R R W D N Q	L A A Y V V S S P	R V A K L R M C	Q Q C V Q L I Q K	M V I V A T L W N	G A K L V I E C K	L S G Q L I	421
LktB	Q M T D T W D B Q	L A S Y V V G S S P	R V T V L A T I G	Q Q C V Q L I Q K	T V M V I T L W L	G A H L V I S G D	L S I G Q L I	412
ApxIB	Q M T H T W D B Q	L A S Y V V S A G P	R V T T L A T I G	Q Q C V Q L I Q K	T V M V I T L W L	G A H L V I S G D	L S I G Q L I	411
HlyB	Q M T H T W D B Q	L A G T V A A G P	R V T V L A T I G	Q Q C V Q L I Q K	T V M V I T L W L	G A H L V I S G D	L S I G Q L I	411
MbxB	A P H M L A G Q V	A A P V I R L A Q	L W Q D F Q Q V G	I S V A R L G D T	L N T P T E R S T	S E L T L P I K	G D I T P E N	482
LktB	A P H M L S G Q V	I A P V I R L A Q	L W Q D F Q Q V G	I S V T R L G D V	L E S P T E Q O Q	G R L S L P H I K	G D I S P E N	473
ApxIB	A P H M L S G Q V	I A P V I R L A Q	L W Q D F Q Q V G	I S V T R L G D V	L H S P T E S I Q	G R L A L P H I K	G D I T P R N	472
HlyB	A P H M L A G Q V	I A P V I R L A Q	L W Q D F Q Q V G	I S V T R L G D V	L H S P T E S Y H	G R L A L P H I K	G D I T F R E	472
MbxB	W D P R Y K I D G	H L I L Q F L N L	O I N A G E F T G	I V G R S G S G K	S T L T K L I Q R	L T P E N G R T	L I D G N D L	543
LktB	I R P R Y K P D A	P T I L H H V S L	E I R Q G E V I G	I V G R S G S G K	S T L T K L I Q R	F T I P E N G Q V	L I D G H D L	534
ApxIB	I R P R Y K P D A	P T I L H D V S L	E I R Q G E V I G	I V G R S G S G K	S T L T K L I Q R	F T I P E N G Q V	L I D G H D L	533
HlyB	I R P R Y K P D S	P T I L D N E N L	E I R Q G E V I G	I V G R S G S G K	S T L T K L I Q R	F T I P E N G Q V	L I D G H D L	533
MbxB	A L A D P A N L R	R Q V G V V V L Q	H V U L L N R S I R	D E I A L T D G	M S . E F I I Q R	A K L A G A H D F	I M B L P E G	604
LktB	A L A D P H W L R	R Q G V V V L Q D	H V U L L N R S I R	D E I A L T D G	M P H E . V V Y A	A K L A G A H D F	I S E L R E G	595
ApxIB	A L A D P H W L R	R Q V G V V V L Q D	H V U L L N R S I R	D E I A L T D G	M P M E K I . . .	A K L A G A H D F	I S E L R E G	594
HlyB	A L A D P H W L R	R Q V G V V V L Q D	H V U L L N R S I R	D E I A L T D G	M S V E R V I T A	A K L A G A H D F	I S E L R E G	594
MbxB	I D T I V G E Q Q	A C L S C G Q R Q	E I A I A R A L M	T N P . I L I P D	E A T S A L D I E	S E R A I M Q R M	Q A I C O G R	665
LktB	I N T I V G E Q Q	A G L S S G G Q R Q	E I A I A R A L V	T N P . I L I P D	E A T S A L D I E	S E H I I M Q R M	Q K I C O G R	656
ApxIB	I N T I V G E Q Q	A G L S S G G Q R Q	E I A I A R A L V	T N P . I L I P D	E A T S A L D I E	S E H I I M R M	H Q I C K G R	655
HlyB	I N T I V G E Q Q	A G L S S G G Q R Q	E I A I A R A L V	T N P . I L I P D	E A T S A L D I E	S E H I I M R M	H Q I C K G R	655
MbxB	T V I I I A H R L	S T V K H A H R I	I A M E G K I V	E Q G T H Q E L L	Q K E D G Y Y R X	L Y D L Q N G	717	SEG ID NO: 18
LktB	T V I I I A H R L	S T V K H A D R I	I V M E K G E I V	E Q G K H H E L L	Q N S H C L Y S Y	L H Q L Q L N	708	SEG ID NO: 19
ApxIB	T V I I I A H R L	S T V K H A D R I	I V M E K G Q I V	E Q G K H K E L L	A D P H G L Y H	L H Q L Q S E	707	SEG ID NO: 20
HlyB	T V I I I A H R L	S T V K H A D R I	I V M E K G R I V	E Q G K H K E L L	S E P E S L Y S Y	L Y Q L Q S D	707	SEG ID NO: 21

FIG. 10

DNASIS Translation Editor [11-00 C gene.dna]

1 ATGACGAAAAAGTTGCAGAGCTAGGTTAATTGCATGGCTTGGCTAACCTGTATG	60
1 M T K K F A E L G L I A W L W S N S D M	20
61 CATAAACATTGGACGTTGTCTTGTGCGACCAATGTTATTCCGGCAATTGAGACAGGT	120
21 H K H W T L S L F A T N V I P A I E T G	40
121 CAATATGTTATATTGAAAAGAGAAGATATGCCGTAGCATATTGAGTTGGCTAAACTT	180
41 Q Y V I L K R E D M P V A Y C S W A K L	60
181 AGTTTAGAAAAGAGGTTAAATATATTAAACGATGTTACTCTCTTAAGTTAGATGACTGG	240
61 S L E N E V K Y I N D V T S L K L D D W	80
241 CAGTCAGGTGACCGAAACTGGTTATTGACTGGATTGCTCCATTGGCGATAGTCTTACA	300
81 Q S G D R N W F I D W I A P F G D S L T	100
301 CTCACAAAACACATGAGAACGTTATTTCAAGATGAATTGTTAGAGCGATTGTAGAT	360
101 L T K H M R T L F S D E L F R A I R V D	120
361 GGAAATTCAATCGATGTAAGATATCTGAATTTATGAAAGTCTGTTGATTCAAATTA	420
121 G N S S H G K I S E F Y G K S V D S K L	140
421 GCCTCAAGAATATTCACAATATCACGAAGATTTGACGAGCAAATTGTCAACTCAGAAT	480
141 A S R I F A Q Y H E D L T S K L S T Q N	160
481 AATTTTATTATATCTAAAGATAATTAA	507
161 N F I I S K D N *	169

^{m6x} C
^{m6x} C
^{m6x} C

FIG. 11

MbxC	---	M T K K F A E	L G L I A W L W S N	S D H K H W T L S	L F A T N V I P A I	E T G Q Y	42
LktC	--	M N Q S Y F N L	L G N I T W L W M N	S S L H K E W S C E	L L A R N V I P A I	E N E Q Y	43
ApxIC	M S K K I N G E F V	L G E V A H L W A S	S P L E R K W P L S	L L A I N V L P A I	E S N Q Y	45	
HlyC	- M N R N N P L E V	L G H V S W L W A S	S P L H R N W P V S	L F A I N V L P A I	R A N Q Y	44	

MbxC	V F L K R D M P V	A Y C S W A K L S L	E N E V K Y I N D V	T S L K L D D W Q S	G D R N W	87
LktC	M L L I D N G I P I	A Y C S W A D L N L	E T E V R V Y I K D I	N S L T P E R W Q S	G D R R W	88
ApxIC	V U L L K R D G F P I	A M C S W A N L N L	E N E I K Y L D D V	A S L V A D D W T S	G D R R W	90
HlyC	A L L T R D N I P V	A Y C S W A N L S L	E N E I K Y L N D V	T S L V A E D W T S	G D R M W	89

MbxC	F I D W I A P F G D	S L T L T K E M R T	L F S D E L F R A I	R V D G N S S . H G	K I S E F	131
LktC	I I D W I A P F G H	S Q L L Y K X M C Q	R K P D M I V R S I	R F Y P R Q K E L G	K I A Y F	133
ApxIC	F I D W I A P F G D	S A A L Y K E M R D	N F P N E L F R A I	R V D P D S R . V G	R I S E F	134
HlyC	F I V W I A P F G D	N G A L Y K E M R K	K F P D E L F R A I	R V D P R T H . V G	R N S E F	133

MbxC	M G K S W D S K L A	S E I F A Q Y H E D	L T S K L L S T Q N N	F I I S K D N -	168
LktC	K G G K D D K R T A	K K R F D T Y Q E E	L A T A L K N E F N	F I K K - - -	167
ApxIC	H G G K I D K K L A	S K I F O Q Y H F E	L M S E L K N K Q N	F K F S L V N S	172
HlyC	H G G K I D K Q L A	N R I P K O Y H E D	L I T E V K N K S D	P N F S L T G -	170

SEQ ID NO: 32
 SEQ ID NO: 33
 SEQ ID NO: 34
 SEQ ID NO: 35

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DNASIS TRANSLATION EDITOR [11-00 v gene.aaa]

60 FIG 12-1

1 ATGTTTATACAAGCACTAAAGATT	TTTATTTCGCTATATAACC	GTTGGCGCAATACA	60
1 M F I Q A L K D F	I R Y I T V W R N T		
61 TGGGCAGTTCGAGACCAACTAACCCCTCCTAAGCGTACTAAAGAAGAACTCGCTTCTT		120	
21 W A V R D Q L T P P K R T K E E L A F L		40	
121 CCTGCACATCTAGAACTCACTGACACACCTGTATCCAGATCTTAAGTGGACAGCTAGA		180	
41 P A H L E L T D T P V S R S S K W T A R		60	
181 ATAATCATGATATTTGCTTATTTGCTATGGTCTGGGTTGGACAGATTGACATT		240	
61 I I M I F V L F A L L W S W V G Q I D I		80	
241 GTTGCTACAGCTTCAGGTAAAATTCTTCAGGTAGCCGTAGCAAGACTATTCAATCTTG		300	
81 V A T A S G K I S S G S R S K T I Q S L		100	
301 GAAACAGCGATAGTTAAAGCAGTTATGTACGTGATGGTCAAATGTTCAACAAGGTGAA		360	
101 E T A I V K A V Y V R D G Q N V Q Q G E		120	
361 ATATTAGTAGATTTAGTGGGATCGGTTAGATAGTGTAGTGTCTAGTCGAGAAAGCC		420	
121 I L V D L V G I G S D S D V A Q S E K A		140	
421 CTTCGAGCGCGCAATTATCTAACGCTACGCCCTGAAGCAATTATCAGCATTAAATCAC		480	
141 L R A A Q L S K L R L E A I L S A L N H		160	
481 CGTATTAATCCTCAGATTGATGTAGCATATGCAAAGTCTTAAATATTCAGAACCGAA		540	
161 R I N P Q I D V A Y A K S L N I S E S E		180	
541 ATTAATGAAGCTCAAACCTTACGCCAAATCAATATCAAGCATGGTTAGCACAAGATGAA		600	
181 I N E A Q T L A Q N Q Y Q A W L A Q D E		200	
601 CAACTAAAATTAAACCTTAAAGGACATCAAGCAGAATTACAATCTGCTCGATCCAGAA		660	
201 Q L K L T L K G H Q A E L Q S A R S Q E		220	
661 CAAAAGTTGGTTTCAAGTTGGTCAATTGAACATCAAAGACTGATGATTATCGGAGTCTC		720	
221 Q K L V S V G A I E H Q K T D D Y R S L		240	
721 AAAGCAGAAAATTATATCTGAGCATGCTTATCTAGAACACAAGAAAGCAAATTACTTAGC		780	
241 K A E N F I S E H A Y L E Q E S K L L S		260	
781 AATCAAAATGATTACAAAGTACACGTAGTCAGATTCAAAAAATACAGGCTGCAATCATG		840	
261 N Q N D L Q S T R S Q I Q K I Q A A I M		280	
841 CAAGCTGAACAGAACCGTATGTTATATACTCAAAATCTAAAACGTGATACTAGAACATCT		900	
281 Q A E Q N R M L Y T Q N L K R D T L E S		300	
901 TTACGCCAACCAATGAACAGATTAATCAATATACTGGTCAAACATAAAAGCTAACAGAG		960	
301 L R Q T N E Q I N Q Y T G Q T N K A K Q		320	
961 CGACAGAAATTGCTGAGTATTAAATCACCTGTTAATGGTACTATACAAGAGCTAACAGCT		1020	
321 R Q K L L S I K S P V N G T I Q E L T A		340	
1021 TATACTTTAGGTGGAGTTGTACAAGCAGCACAAAAATTATGGTGTGGCACCTAACGAT		1080	
341 Y T L G G V V Q A A Q K I M V V A P N D		360	
1081 AATCAAGTGGAAAGTAGAGGTATTAGTGTAAATAAGATATCGGCTTGTAAAAGCTGGG		1140	
361 N Q V E V E V L V L N K D I G F V K A G		380	
1141 CAGAATGTTATCATCAAATCGAGAGTTCTTATACACGTTATGGTTATTAACAGGT		1200	
381 Q N V I I K I E S F P Y T R Y G Y L T G		400	
1201 AAAATAAAAAGTATTAGTCATGATGCTATAGAACATCAACATTAGGTCTAGTGTACT		1260	
401 K I K S I S H D A I E H Q H L G L V Y T		420	
1261 GCACTTGTTCTCTGATAAAAGCACATTAATATAGATGGAGTAACAATCAACTAACG		1320	
421 A L V S L D K S T L N I D G V T I N L T		440	

UNASIS TRANSLATION FOLLOWING THE 1320 POSITION
1321 CCAGGAATGAATGTTACTGCTGAAATTAAAACAGGTAAACGTCGTGTTGGATTATATA 1380
441 P G M N V T A E I T G K R R V L D Y I
1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTCGAGAACGCTAA 1428
461 L S P L Q T K V D E S F R E R * 476

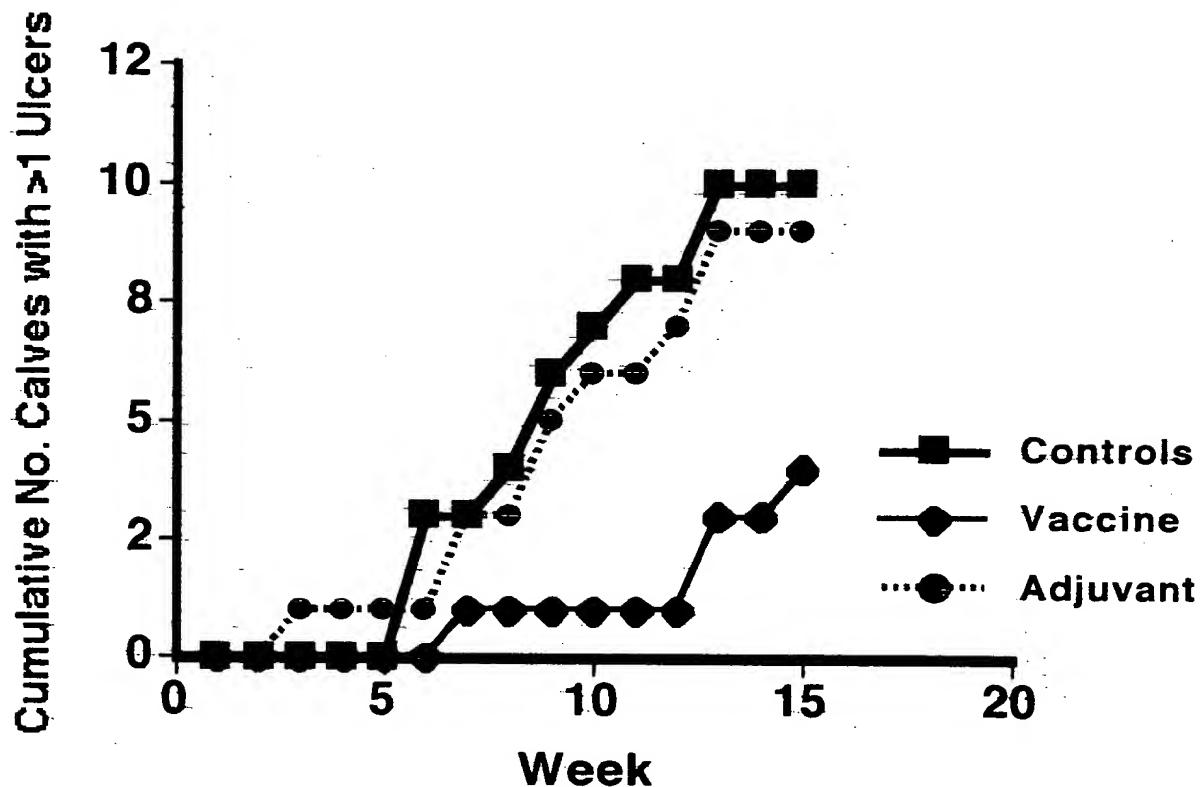
FIG. 12-2

FIG. 13

MbxD	- - M F I Q A L K	F F I R Y I T V W R	N T W A F R D Q L T	P P K R T K E L A	F L P A H E L T	48
LktD	M K I W L S G I Y E	F F L R Y K N I W A	S V W K I R K I L D	H P N R K R D E S E	F L P A H E L I E	50
ApxID	M K T W L M G L Y E	F F Q R Y R T V W T	E I W K I R H Q L D	T P D R E K D E N E	F L P A H E L I E	50
HlyD	M K T W L M G F S E	F L L R Y R L V W S	E T W K I R K Q L D	T P V R E K D E N E	F L P A H E L I E	50
MbxD	T P V S R S S W T	A R G I M I F V L F	A L L W S W V G Q	E I V A T A S G K	S S G S R S K T I Q	98
LktD	T P V S K K P R L I	A Y L I M L F L V V	A A V L A S V S K V	E I V A T A P G K L	T F S G R S K E I K	100
ApxID	T P V S K K P R L I	A Y L I M L F L F L	A L V S I V S H V	E I V A T A T G K L	A F S D R S K E I K	100
HlyD	T P V S R P P R L I	A Y F I M G P L V I	A F A L S V L G Q V	E I V A T A N G K L	T I S G R S K E I K	100
MbxD	S I E T A I V K A	F V V D G Q N V I Q	G C E L V D L V G	G S D S D V A Q S E	K A L R A R Q L S K	148
LktD	P I E N A I V Q E I	F V K D G Q F V E K	G Q L L V S L T A L	G S D A D I K K T M	A S L S L A K L E N	150
ApxID	P I E N A V K E I	F V Q D G Q F V E K	D Q L L L H L T A L	G A D A D Q K T K	S S L S L T K L E R	150
HlyD	P I E N S I V K E I	I V K A G S V R K	G D V L L K L T A L	G A A D T L K T Q	S S L L Q R A L E Q	150
MbxD	L R L E A I L S A	N H R I N P Q I D V	A Y A K S L . N I S	E S E I N E A Q T L	A Q N Q Y Q A W L A	197
LktD	Y R Y Q T I I L T A I	E K E S I L P V I D L	. S R T E F K D S S	E E D R L R I K H L	I T E Q Y T T W Q R	199
ApxID	Y R Y E T I I L E A	A A D R L P F L I L	. T K D E F K R A T	E E D K T R I Y R L	I T E Q F E A W Q R	199
HlyD	I R Y Q I I L S R S I	E L N K L P E E K L	P D E P Y F Q N V S	E E E V L R I T S L	I K E Q F S T W Q N	200
MbxD	Q D E Q L K L T L K	G H I A E L Q S A R	S Q E Q K L V S V G	A I E H G K T D D	R S L K A E N F I S	247
LktD	Q K T Q K T L A Y K	R K E A E K Q T I F	A Y F R K Y E G A T	R I E Q E K L K D F	K A L Y K Q K S I S	249
ApxID	Q K Y Q K E L A L Q	R E E A E K Q T L	A N I R K Y E G I S	R V E N E R L K K D L	K K L F N S K S T S	249
HlyD	Q K Y Q K E L N L D	E K R A E E L T I L	A R I N Y E N V S	R V E K S R L D D F	R S L L H K Q A I A	250
MbxD	E H A Y L E Q E S K	L I F S N Q N J L Q S	T R S Q N Q K I I A	A I I Q A E W N R M	L Y T Q N L K R D T	297
LktD	K H E L L A Q E N K	L I E A Q N A V A V	Y R S K L N E E E N	D L L N V K E E L E	L I T Q F F R S D T	299
ApxID	K H D V L T Q E N	H I E A V N H E L A V	Y K S R L N E E E S	D L R Q A K E E I H	L I T Q L F F A D I	299
HlyD	K H A V L E Q E N K	Y K E A A N E L R V	Y K S Q L E V I E S	W I L S A K E E Y Q	L I T Q L F R N I I	300
MbxD	L E S L R Q T N E Q	I N Q Y T G E T N K	A K Q R Q K L L S I	F S P V N G T I Q	L T A T T L G G V V	347
LktD	L E K L K Q H I E N	E R Q L R L E L E K	N N Q R R Q A S M I	R A P V S G T V Q Q	L K I H T I G G V V	349
ApxID	L E K L K Q N V E A	E K Q L S L E L E K	N E Q R Q I A S V I	R A P V S G T V Q Q	L K T H T V G G V V	349
HlyD	L E K L R Q T T E S	I E L L T L E L E K	N E R Q Q A S V I	R A P V S G K V Q Q	L K V H T E G G V V	350
MbxD	Q A A E K I M V V A	P N D N Q V E V E V	L U V L H K D I G F V	K A G Q N V I I K V	E S F P P Y T R Y G Y	397
LktD	T T A E T L M I V	P E D D V L E A T A	L U P H K D I G F V	A A G Q E V I I K V	E T F P P Y T R Y G Y	399
ApxID	T T A E T L M V I A	P E D D V L E V T A	L U Q N K D I G F I	E V G Q D A I I K V	E T F P P Y T R Y G Y	399
HlyD	T T A E T L M V I V	P E D D T L E V T A	L V Q N K D I G F I	N V G Q N A I I K V	E A F P P Y T R Y G Y	400
MbxD	L T G K I K S I S H	D A I E H Q H L G L	V M T A Z V S F D	S T L N . I D G V T	I N L T P G M N V T	446
LktD	L T G I I K H I S P	D A I E Q P N V G L	V F N A T I A I D R	H N L T S P D G E K	I D L L S S G M T T	449
ApxID	L M G K V K N I T L	D A I E H P Q L G L	V F N S I I S I D R	K T L S G K D G K E	I E L G S G M S V T	449
HlyD	L V G K V K N I N L	D A I E D Q K L G L	V P N V I V S S A E	N D L S T . G N K H	I P L S S G M A V T	449
MbxD	A E I K T G K R R V	E D Y T L S P L I T	K V D E S F R E R	475	SEQ ID NO: 37	
LktD	A E I K T G E R S V	M S Y L L S P L E E	S V T E S L R E R	478	SEQ ID NO: 38	
ApxID	A E I K T G E R S V	I S Y L L S P L E E	S V S E S L R E R	478	SEQ ID NO: 39	
HlyD	A E I K T G M R S V	I S Y L L S P L E E	S V T E S L H E R	478	SEQ ID NO: 40	

F16.14

Cumulative Number of Calves With Severe Ulcers



Number of calves with ulcers with clinical scores >+2

FIG 15

Number of calves affected each week

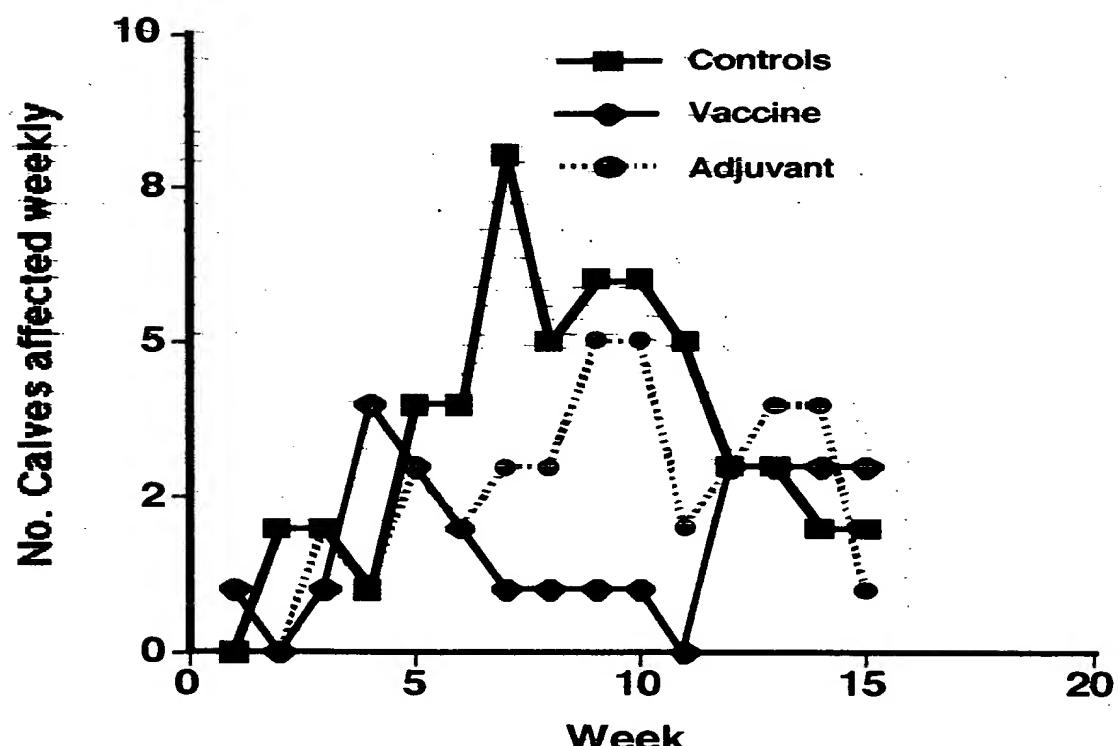
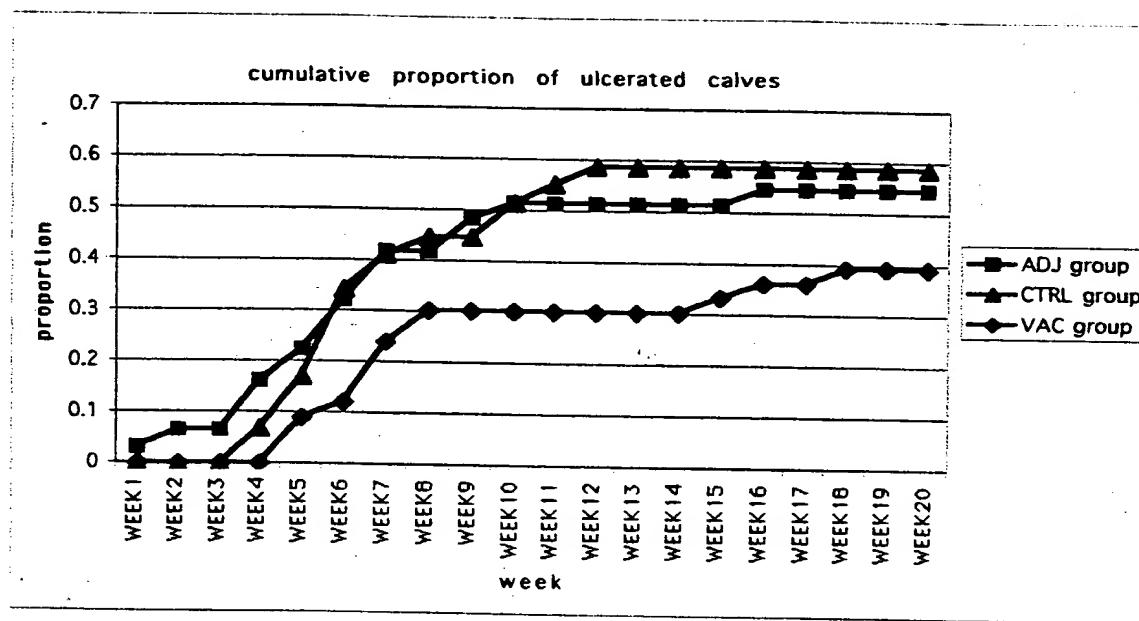


Figure 15

Number of calves affected weekly in 1 group of vaccinated calves and in controls.

FIG. 16

Cumulative proportion of ulcerated calves during the trial. Calves received as vaccines either saline (designated 'CTRL'), adjuvant alone (designated 'ADJ'), or the recombinant cytotoxin vaccine (designated 'VAC').

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